

Package ‘CIhdq’

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Type Package

Title Regularized projection score estimation of treatment effects in high-dimensional quantile regression

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Depends R (>= 3.1.0)

Imports glmnet, grpreg, SparseM, quantreg

Description A regularized projection score method is proposed for estimating treatment effects in quantile regression in the presence of high-dimensional confounding covariates. This method is based on an estimated projection score function of the low-dimensional treatment parameters in the presence of high-dimensional confounding covariates. We propose one-step algorithm and a refitted wild bootstrapping approach for variance estimation. This enables us to construct confidence intervals for the treatment effects in the high-dimensional circumstances.

License GPL-2

LazyData true

NeedsCompilation yes

Repository GitHub

URL <https://github.com/xliusufe/CIhdq>

Encoding UTF-8

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CIhdq-package	<i>Regularized projection score estimation of treatment effects in high-dimensional quantile regression</i>
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Description

A regularized projection score method is proposed for estimating treatment effects in quantile regression in the presence of high-dimensional confounding covariates. This method is based on an estimated projection score function of the low-dimensional treatment parameters in the presence of high-dimensional confounding covariates. We propose one-step algorithm and a refitted wild bootstrapping approach for variance estimation. This enables us to construct confidence intervals for the treatment effects in the high-dimensional circumstances.

Details

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References

Feng, X., Huang, J. and Liu, X. (2019). Regularized projection score estimation of treatment effects in high-dimensional quantile regression. Manuscript.

infern	<i>Provide CI of individual coefficient of high-dimensional quantile regression.</i>
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Description

This function provides the confidence intervals of individual coefficient of high-dimensional quantile regression by a regularized projection score method for estimating treatment effects. One-step estimation procedure can speed up computation, and the Bootstrap method can narrow the length of CI.

Usage

```
infern(y, x, z, tau, method="OneStep", pen, eps=1e-6, level=0.85, iter.num=100, RCV=F, K=1, weights=NULL, B
```

Arguments

<code>y</code>	The response, a vector of size n
<code>x</code>	The treatment effects, a matrix with dimension $n \times p$
<code>z</code>	The confounders a matrix with dimension $n \times q$
<code>tau</code>	The given quantile, a scale in the unit interval
<code>method</code>	The method including "OneStep", "Iterative". "OneStep" denotes one-step method (Feng et al. 2019); "Iterative" denotes that the iteration stops when algorithm converges. Default is "OneStep".
<code>pen</code>	The penalty including "glasso" and "lasso". "glasso" denotes the grouped lasso that is used in the regression of treatment effect on confounders; "lasso" denotes the lasso. Default is "glasso".
<code>eps</code>	The perturbation when the proposed algorithm is used. Default is $\epsilon=1e-6$.
<code>level</code>	The length of tuning parameter α which is selected automatically. Default is 50.
<code>iter.num</code>	The number of folds for the tuning selection by CV. Default is 5.
<code>RCV</code>	Use refitted cross validation method and wild bootstrap to estimate the asymptotic covariance matrix. Default is False.
<code>K</code>	The number of repeated RCV. Default is 1.
<code>weights</code>	The weights used for wild bootstrap; if not specified (=NULL). Default is NULL.
<code>B</code>	The size for bootstrap. Default is 1000.

Value

<code>est</code>	Estimator of β . It is a list.
<code>cov</code>	Covariance matrix of β . It is a $d \times d$ -matrix.

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References

Feng, X., Huang, J. and Liu, X. (2019). Regularized projection score estimation of treatment effects in high-dimensional quantile regression. Manuscript.

Examples

```
n <- 50
d <- 3
s <- 3
p <- 20
beta <- rep(3,d)
eta <- c(rep(3,s),numeric(p-s))
x <- matrix(rnorm(n*d),n,d)
z <- matrix(rnorm(n*(p-1)),n,p-1)
y <- x
fit <- infern(y,x,z,tau=tau,B=500)
ests <- fit$result
est.coef <- cbind(est.coef,ests$coef)
boot.var <- diag(fit$cov)
lbounds <- ests$coef-qnorm((1+alpha)/2)*sqrt(boot.var)
```

```
ubounds <- ests$coef+qnorm((1+alpha)/2)*sqrt(boot.var)
counts <- ifelse(lbounds<beta&beta<ubounds,1,0)
coverage <- cbind(coverage,counts)
```

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